CERTIFICATE OF MAILING

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Steven L. Highlander

PATENT

45

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Gary L. Clayman

Serial No.: 08/758,033

Filed: November 27, 1996

For: METHODS AND COMPOSITIONS FOR

THE DIAGNOSIS AND TREATMENT OF

CANCER

Group Art Unit: 1804

Examiner: Unknown

Atty. Dkt. No.: INGN:041/HYL

STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(f)

BOX SEQUENCE

Assistant Commissioner for Patents Washington, D.C. 20231

Sir:

Submitted herewith is a computer readable form and a paper copy of the sequence listing of those sequences in the captioned patent application. The computer readable form of the sequence listing is the same as the paper copy of the sequence listing. The sequence information provided in the Specification is also the same as the sequence listing of the enclosed computer readable and paper forms of the sequence listing.

A: 99269(24LH01!.DOC)

Respectfully submitted,

Seven L. Highlander

Reg. No. 37,642

Attorney for Applicant

ARNOLD, WHITE & DURKEE P.O. Box 4433 Houston, Texas 77210-4433 (512) 418-3000

Date: April 8, 1997

RAW SEQUENCE LISTING PATENT APPLICATION US/08/758,033A

DATE: 05/14/97 TIME: 12:59:36

INPUT SET: S17693.raw

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This Raw Listing contains the General Information Section and up to the first 5 pages.

1	•	SEQUENCE LISTING
2		
3	(1) Ge	eneral Information:
4		" C D ~
5 6	(i)	SEQUENCE LISTING eneral Information: APPLICANT: Clayman, Gary L. TITLE OF INVENTION: Methods and Compositions for the
7	(ii)	TITLE OF INVENTION: Methods and Compositions for the
8	(/	Diagnosis and Treatment of Cancer
9		· · · · · · · · · · · · · · · · · · ·
10	(iii)	NUMBER OF SEQUENCES: 14
11		
12	(iv)	CORRESPONDENCE ADDRESS:
13		(A) ADDRESSEE: Arnold, White & Durkee
14		(B) STREET: P.O. Box 4433
15		(C) CITY: Houston
16		(D) STATE: TX
17		(E) COUNTRY: USA
18		(F) ZIP: 77057-4433
19		### ##################################
20	(4)	COMPUTER READABLE FORM:
21 22		(A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible
22		(C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 24		(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25		(D) BOTTWARE: Fatencin Release #1.0, Version #1.30
26	(vi)	CURRENT APPLICATION DATA:
27	(• =)	(A) APPLICATION NUMBER: US 08/758,033
28		(B) FILING DATE: 27-NOV-1996
29	•	(C) CLASSIFICATION:
30		• •
31	(viii)	ATTORNEY/AGENT INFORMATION:
32		(A) NAME: Highlander, Steven L.
33		(B) REGISTRATION NUMBER: 37,642
34		(C) REFERENCE/DOCKET NUMBER: INGN:041
35		
36	(ix)	TELECOMMUNICATION INFORMATION:
37		(A) TELEPHONE: (512) 418-3000
38		(B) TELEFAX: (713) 789-2679
39		
40	/0\ TNEO	DANKED HOD CHO ID NO.1.
41	(2) INFO	RMATION FOR SEQ ID NO:1:
42 43	(3)	SEQUENCE CHARACTERISTICS:
43 44	(+)	(A) LENGTH: 2066 base pairs
45		(B) TYPE: nucleic acid
46		(C) STRANDEDNESS: single
		, -,

RAW SEQUENCE LISTING PATENT APPLICATION US/08/758,033A

DATE: 05/14/97 TIME: 12:59:40

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
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CTGCCCTGTG CAGCTGTGGG TTGATTCCAC ACCCCCGCCC GGCACCCGCG TCCGCGCCAT	180
GGCCATCTAC AAGCAGTCAC AGCACATGAC GGAGGTTGTG AGGCGCTGCC CCCACCATGA	240
GCGCTGCTCA GATAGCGATG GTCTGGCCCC TCCTCAGCAT CTTATCCGAG TGGAAGGAAA	.300
TTTGCGTGTG GAGTATTTGG ATGACAGAAA CACTTTTCGA CATAGTGTGG TGGTGCCCTA	360
TGAGCCGCCT GAGGTTGGCT CTGACTGTAC CACCATCCAC TACAACTACA TGTGTAACAG	420
TTCCTGCATG GGCGGCATGA ACCGGAGGCC CATCCTCACC ATCATCACAC TGGAAGACTC	480
CAGTGGTAAT CTACTGGGAC GGAACAGCTT TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG	540
AGACCGGCGC ACAGAGGAAG AGAATCTCCG CAAGAAAGGG GAGCCTCACC ACGAGCTGCC	600
CCCAGGGAGC ACTAAGCGAG CACTGCCCAA CAACACCAGC TCCTCTCCCC AGCCAAAGAA	660
GAAACCACTG GATGGAGAAT ATTTCACCCT TCAGATCCGT GGGCGTGAGC GCTTCGAGAT	720
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TCCCGGGGCT CCACTGAACA AGTTGGCCTG CACTGGTGTT TTGTTGTGGG GAGGAGGATG	1080
GGGAGTAGGA CATACCAGCT TAGATTTTAA GGTTTTTACT GTGAGGGATG TTTGGGAGAT	1140
GTAAGAAATG TTCTTGCAGT TAAGGGTTAG TTTACAATCA GCCACATTCT AGGTAGGGGC	1200
CCACTTCACC GTACTAACCA GGGAAGCTGT CCCTCACTGT TGAATTTTCT CTAACTTCAA	1260
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AATGAAATAATGTACATCTG GCCTTGAAAC CACCTTTTAT TACATGGGGT CTAGAACTTG	1380
ACCCCCTTGA GGGTGCTTGT TCCCTCTCCC TGTTGGTCGG TGGGTTGGTA GTTTCTACAG	1440

TTGGGCAGCT GGTTAGGTAG AGGGAGTTGT CAAGTCTCTG CTGGCCCAGC CAAACCCTGT 1500

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101	CTGACAAC	CT C	l'TGG'	rgaa(CT	raga'	rcct	AAA	AGGA	TAA	GTCA	CCCC.	AT C	CCAC.	ACCC'	r	1560
102																	
103	GGAGGATT	rc a'	rctc'	rtgt <i>i</i>	A TAC	GATG	ATCT	GGA'	rcca(CCA .	AGAC'	rtgt'	TT T	AGCT	CAGG	G	1620
104																	
105	TCCAATTT	CT T	TTTT(CTTTT	r TT	r TTT	PTTT	TTT	CTTT	rtc '	TTTG.	AGAC'	TG G	GTCT(CTTT	3	1680
106																	
107	TTGCCCCA	GG C	rgga(GTGG <i>i</i>	A GT	GCG'	IGAT	CTG	GCTT/	ACT	GCAG	CCTT'	TG C	CTCC	CCGG	C	1740
108																	
109	TCGAGCAG	rc c'	rgcc'	rcag(CTC	CCGG	AGTA	GCT	GGGA(CCA	CAGG'	TTCA'	rg c	CACC	ATGG	C	1800
110																	
111	CAGCCAAC	rt t	rgca'	rgtti	TG:	raga(GATG	GGG'	rctc2	ACA	GTGT'	rgcc	CA G	GCTG	GTCT	C	1860
112																	
113	AAACTCCT	GG GG	CTCA	GCG <i>I</i>	A TC	CACC	rgtc	TCA	GCCT	CCC .	AGAG'	rgct	GG G	ATTA	CAAT!	r	1920
114																	
115	GTGAGCCAG	CC AC	CGTC	CAGC	r GG	AAGG	GTCA	ACA'	rctt'	rta (CATT	CTGC	AA G	CACA'	TCTG	C	1980
116																	
117	ATTTTCAC	CC C	ACCC'	TTCC	CT	CTTC	rccc	TTT	TAT	ATC	CCAT'	rttt.	AT A	rcga'	TCTC	Г	2040
118																	
119	TATTTTAC	AA T	AAAA	CTTTC	CT	CCA											2066
120																	
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122	(2) INFO	RMAT:	ION 1	FOR S	SEQ :	ID NO	0:2:										
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124	(i)	~		E CHA													
125		•	•	NGTH:				acid	5								
126			-	PE: a													
127			•	RANDE			_	Te									
128		(D) TOI	POLOC	3Y: .	Linea	ar										
129		~=~						- T									
130	(xi)	SEQ	JENCI	E DES	CKI	LTO	N: 51	EĞ T	U NO	: 2 :							
131	T	m1	m	a 1 -	a1	~	m	a1	Db.	3	T	a1	mh a	T	77.i ~	C	
132 133	Lys 1	THE	туг	GIN	<u>сту</u>	ser	Tyr	GIY	Pne	_	геп	GTA	Pne	Leu	His 15	ser	
134					3					10					13		
135	G1	mbr	212	T ***	Cor	v. l	Πh ~	Crrc	mb v	Петъ	Cor	Dro	λΙο	T 011	Asn	Twe	
136	СТУ	THE	Ата	LуS 20	Ser	vат	THE	Cys	25	туг	Ser	PIO	Ата	30	ASII	гуѕ	
136				20					25					30			
138	Mot	Dho	Cue	Gl n	T 011	λla	Lvc	Пhr	Cue	Dro	Val	Gl n	Lan	Trn	Val	λen	
139	Mec	Pile	35	GTII	пеп	АТА	гуз	40	Cys	PIO	Val	GIII	45	пр	val	ASP	
140			33					40					43				
141	Sor	Thr	Dro	Bro	Dro	@1 ₁₇	Thr	λrα	Val	λτα	λΊэ	Mot	λla	т1Д	Tyr	Tve	
142	Ser	50	110	FIO	FIO	GLY	55	AL 9	V CL	Arg	ALG	60	AIG	116	1 7 1	БУЗ	
143		30					33					00					
144	aln	Sor	Gln	Hic	Mot	Thr	@lu	Va1	Val	Ara	λra	Cue	Dro	Hic	His	Glu	
145	65	261	GIII	птэ	Mec	70	GIU	Val	Val	ALG	75	Суз	FIO	nrs	III	80	
146	65					, 0					, 5		•			00	
147	Ara	Cve	Ser	Aen	Ser	Aen	ឲ្យស	T.em	Δls	Pro	Pro	Gln	Hie	T.e.:	Ile	Δra	
148	AIG	Cys	Ser	voh	85	rah	GLY	Ted	лта	4 0	110	0111	1113	Leu	95	419	
149					0.5										,,		
150	(ev	Glu	ឲ្យស	Δan	T.e.:	Δra	Va1	Glu	ጥህዮ	I.e.i	Asn	Agn	Δra	Agn	Thr	Phe	
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Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp 115 115 120 120 125 125 125 125 125 125 126 125
155 120 125 126 125 156 157 130 135 140 140 157 130 135 140 140 140 157 140 140 140 157 140 140 140 145 150 155 160 145 150 155 160 160 165 165 160 165 170 175 160 161 162 Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val Arg Val Cys Ala 165 165 170 175 175 166 167 166 167 16
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167 168 Cly Clu Pro His His Clu Leu Pro Pro Cly Ser Thr Lys Arg Ala Leu 169 170 171 Pro Asn Asn Thr Ser Ser Ser Pro Cln Pro Lys Lys Lys Pro Leu Asp 172 210 215 220 173 174 Cly Clu Tyr Phe Thr Leu Cln Ile Arg Cly Arg Clu Arg Phe Clu Met 175 225 230 235 240 176 177 Phe Arg Clu Leu Asn Clu Ala Leu Clu Leu Lys Asp Ala Cln Ala Cly 178 245 250 255 180 180 Lys Clu Pro Cly Cly Cly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Cly Cln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Clu 184 275 280 285 185 186 Cly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
168
169
170 171
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173 174
Cly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu Arg Phe Glu Met 225 230 235 240 240 235 240 240 235 240 240 235 240 240 235 235 240 240 235 235 240 240 235 235 235 240 245 245 250 255
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176 177 Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly 178 245 250 255 179 180 Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 285 185 186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp Ala Gln Ala Gly 245 179 180 Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 280 285 185 186 Gly Pro Asp Ser Asp 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2066 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
178 179 180 Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 285 185 186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
179 180 Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 285 185 186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
Lys Glu Pro Gly Gly Ser Arg Ala His Ser Ser His Leu Lys Ser Lys 181 260 265 270 182 183 Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 285 185 186 Gly Pro Asp Ser Asp 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
181
182 183
Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met Phe Lys Thr Glu 184 275 280 285 185 186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
184
185 186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
186 Gly Pro Asp Ser Asp 187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
187 290 188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
188 189 190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
190 (2) INFORMATION FOR SEQ ID NO:3: 191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
191 192 (i) SEQUENCE CHARACTERISTICS: 193 (A) LENGTH: 2066 base pairs 194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
(A) LENGTH: 2066 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (XI) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
194 (B) TYPE: nucleic acid 195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
195 (C) STRANDEDNESS: single 196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
196 (D) TOPOLOGY: linear 197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
197 198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: 199
199
200 CAAAACTTAC CAGGGCAACT ATGGCTTCCA CCTGGGCTTC CTGCAGTCTG GGACAGCCAA 60
201
202 GTCTGTTATG TGCACGTACT CTCCTCCCCT CAATAAGCTA TTCTGCCAGC TGGCGAAGAC 120
203
204 GTGCCCTGTG CAGTTGTGGG TCAGCGCCAC ACCTCCAGCT GGGAGCCGTG TCCGCGCCAT 180

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